AMENDMENT TO THE CLAIMS:

This listing of claims will replace all prior listings of claims in the application:

LISTING OF CLAIMS:

1-234 were cancelled in a Preliminary Amendment dated December 2, 2003.

Clams 235-271 are cancelled herein.

272. (New) A method for identifying a compound that putatively modulates or elicits taste in a human subject comprising:

(1) screening one or more compounds in a binding assay which identifies compounds that specifically bind to a human T1R1 polypeptide or which modulate (inhibit or enhance) the specific binding of another compound that specifically binds to said human T1R1 polypeptide, wherein said T1R1 polypeptide is selected from the group consisting of:

(a) a human T1R1 polypeptide having the amino acid sequence encoded by SEQ. ID. NO: 17;

(b) a human T1R1 polypeptide encoded by a nucleic acid sequence that specifically hybridizes to the hT1R1 nucleic acid sequence contained in SEQ. ID. NOS: 15 or 16 under stringent hybridization conditions which are 50% formamide, 5X SSC and 1% SDS, incubating at 65 degrees C; with wash in 0.2X SSC and 0.1% SDS at 65 degrees C and which human T1R1 polypeptide is specifically bound by at least one taste modulatory compound that specifically binds to the human T1R1 polypeptide contained in SEQ. ID NO:17; and

(c) a human T1R1 polypeptide which has possesses at least 90% sequence identity to the amino acid sequence contained in SEQ. ID. NO:17 and which specifically binds to

at least one taste modulatory compound which specifically binds to the native T1R1 polypeptide contained in SEQ ID NO:17;

(2) identifying compounds that putatively modulate taste based on its specific binding to a human T1R1 polypeptide according to (a), (b), or (c), or its modulation (inhibition or enhancement) of the specific binding of another compound to a T1R1 polypeptide according to (a), (b), or (c).

273. (New) The method of claim 272, wherein the human T1R1 polypeptide has the amino acid sequence contained in SEQ. ID. NO: 17.

274. (New) The method of claim 272, wherein said T1R1 polypeptide possesses at least 90% sequence identity to the polypeptide contained in SEQ. ID. NO: 17.

275. (New) The method of claim 272, wherein said T1R1 polypeptide possesses at least 95% sequence identity to the polypeptide contained in SEQ. ID. NO:17.

276. (New) The method of claim 272, wherein the T1R1 polypeptide possesses at least 96% sequence identity to the polypeptide contained in SEQ. ID. NO:17.

277 (New) The method of claim 272, wherein the T1R1 polypeptide possesses at least 97% sequence identity to the polypeptide contained in SEQ. ID. NO:17.

278. (New) The method of claim 272, wherein said T1R1 polypeptide possesses at least 98% sequence identity to the polypeptide contained in SEQ. ID. NO:17.

279. (New) The method of claim 272, wherein said T1R1 polypeptide possesses at least 99% sequence identity to the polypeptide contained in SEQ. ID. NO:17.

280. (New) The method of claim 272, wherein said T1R1 polypeptide is encoded by a nucleic acid sequence that hybridizes to the nucleic acid sequence contained in SEQ. ID. NO: 15 or 16 under said stringent hybridization conditions.

281. (New) The method of claim 272, wherein said T1R1 polypeptide is encoded by a sequence that is contained on an expression vector.

282. (New) The method of claim 272, wherein said T1R1 polypeptide is attached to a solid phase.

283. (New) The method of claim 272, wherein said T1R1 polypeptide is in solution.

284. (New) The method of claim 272, wherein T1R1 polypeptide is in a lipid bilayer or vesicle.

285. (New) The method of claim 272, wherein said T1R1 polypeptide is expressed by a cell.

286. (New) The method of claim 272, wherein said T1R1 polypeptide is comprised on a cell membrane.

287. (New) The method of claim 285, wherein the cell is a prokaryotic cell.

288. (New) The method of claim 285, wherein the cell is a eukaryotic cell.

289. (New) The method of claim 285, wherein said cell is a yeast, insect, amphibian or mammalian cell.

290. (New) The method of claim 285, wherein the cell is a CHO cell, HEK-293 cell, COS cell or a Xenopus oocyte.

291. (New) The method of claims 272, wherein the binding assay detects a change in T1R1 polypeptide conformation upon binding of the compound.

292. (New) The method of claim 291, wherein said change in conformation is detected by NMR spectroscopy.

293. (New) The method of claim 291, wherein said change is detected by fluorescence spectroscopy.

294. (New) The method of claim 285, wherein said cell further expresses a G protein that couples to said T1R1 polypeptide.

295. (New) The method of claim 294, wherein said G protein is $G_{\alpha 15}$ or $G_{\alpha 16}$ or gustducin.

296. (New) The method of claim 272, wherein the binding assay includes the use of a label.

297. (New) The method of claim 272, wherein said label is an enzyme, radionuclide, chemiluminescent compound or fluorescent compound.

298. (New) The method of claim 272, wherein the binding assay detects binding of a labeled ligand to said T1R1 polypeptide.

299. (New) The method of claim 272, wherein said assay is a fluorescent polarization or FRET assay.

300. (New) The method of claim 272, wherein binding of a compound to T1R1 polypeptide is detected by a competitive binding assay.

301. (New) The method of claims 272, wherein the binding of a compound to said T1R1 polypeptide is detected by a non-competitive binding assay.

302. (New) The method of claim 272, wherein the binding assay uses an intact or permeabilized cell that expresses said T1R1 polypeptide.

303. (New) The method of claim 272, wherein the binding assay detects release of a labeled ligand from said T1R1 polypeptide.

304. (New) The method of claim 272, wherein the binding assay detects binding of a compound to T1R1 based on a detectable change in fluorescent absorbance or refractive index.

305. (New) The method of claim 272 which is a high throughput binding assay.

306. (New) The method of claim 305 which screens a library of at least 1000 compounds.

307. (New) The method of claim 306, wherein said library is a combinatorial chemical library.

308. (New) The method of claim 272, which further includes step (3) whereby the effect of said putative taste modulating compound is confirmed in a human taste test.